

# Systematic Gene Search in the Incyte LifeSeq Database

Normal tissue  
-50,000 individual ESTs

Tumor tissue  
-50,000 individual ESTs

Priority list  
High

Prostate  
Breast  
Ovary  
Bladder  
Uterus

Iterative assembling  
with  
increasing mismatch

Low

-8,000 contigs  
+  
-25,000 singletons

-8,000 contigs  
+  
-25,000 singletons

## Comparison of databases

normal tissue-  
specific  
(expected: 100-500)

nonspecifically  
expressed genes

tumor tissue-  
specific  
(expected: 100-500)

Genes of Interest

Figure 1

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## Systematische Gen-Suche in der Incyte LifeSeq Datenbank

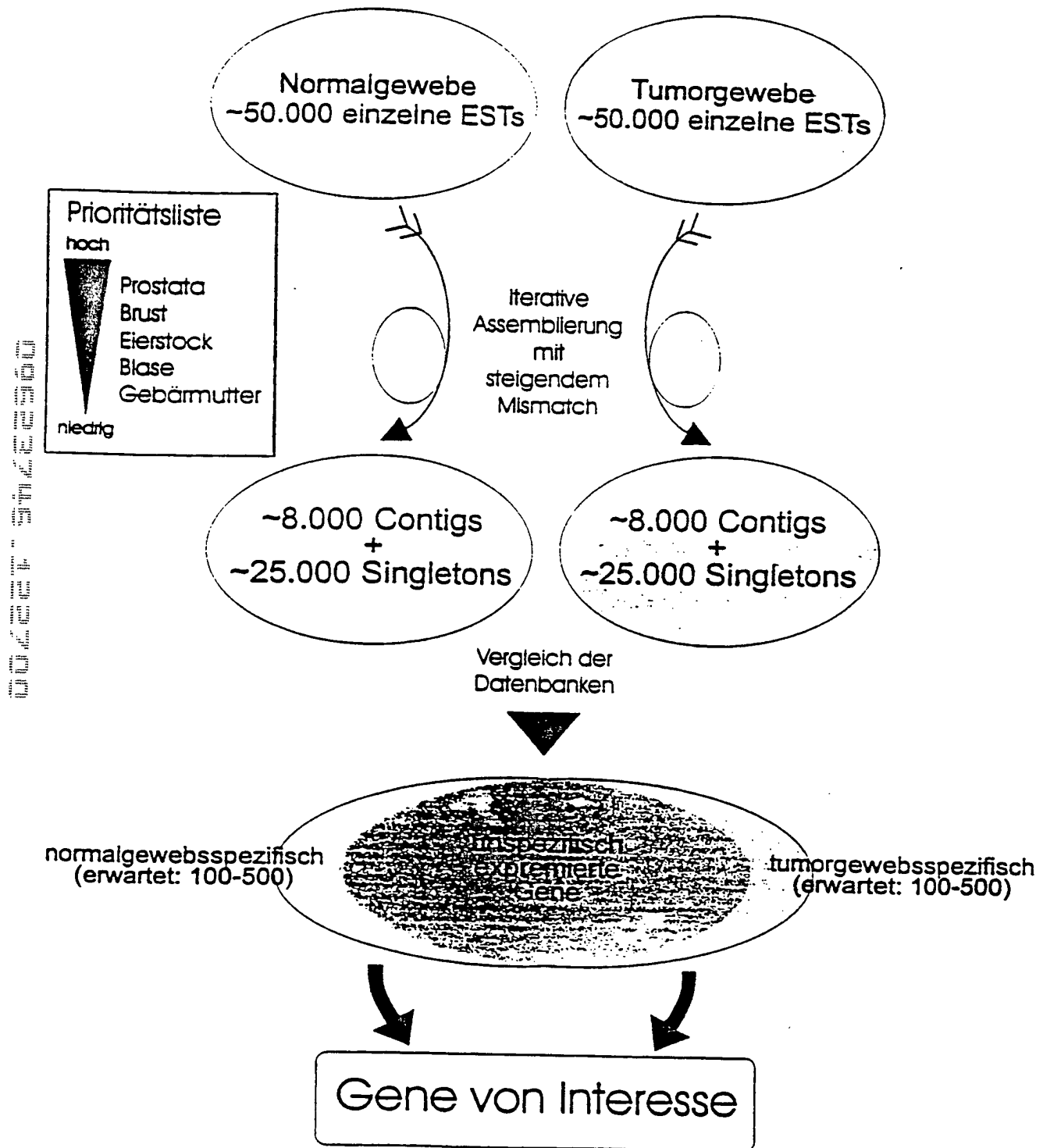


Fig. 1

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## Principle of EST Assembly

-50,000 ESTs per tissue

Assembly at 0% mismatch  
with GAP4 (Staden)

Contigs

Singletons

Contigs increasing in  
number and lengthIterative assembly with  
increasing mismatch  
(1%, 2%, 4%)

5000-6000 contigs

-25,000 other  
singletons-30,000 consensus-  
sequences per tissue

Figure 2a

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# Prinzip der EST-Assemblierung

~50.000 ESTs pro Gewebe

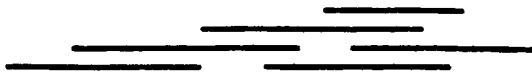


Assemblierung bei 0% Mismatch  
mit GAP4 (Staden)

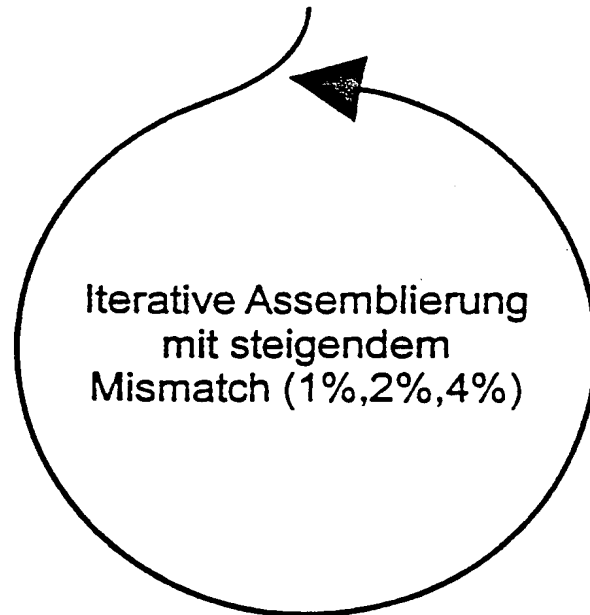


Contigs

Singletons



In Anzahl und Länge  
zunehmende Contigs



5000-6000 Contigs    ~25.000 übrige Singletons



~30.000 Konsensus-  
sequenzen pro Gewebe

Fig. 2a

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-50,000 ESTs of a tissue (e.g.: uterus tumor)

GAP4 Assembly 1st Round:  
minimum initial match: 20  
maximum pads per read: 8  
maximum percent mismatch: 0

GAP4 Database 1  
Contigs 1  
Singletons 1

unassembled  
ESTs

GAP4 Assembly 2nd Round:  
minimum initial match: 20  
maximum pads per read: 8  
maximum percent mismatch: 1

GAP4 Database 2  
Contigs 2  
Singletons 2

unassembled  
ESTs

GAP4 Assembly 3rd Round:  
minimum initial match: 20  
maximum pads per read: 8  
maximum percent mismatch: 2

GAP4 Database 3:  
Contigs 3  
Singletons 3

unassembled  
ESTs

Figure 2b1

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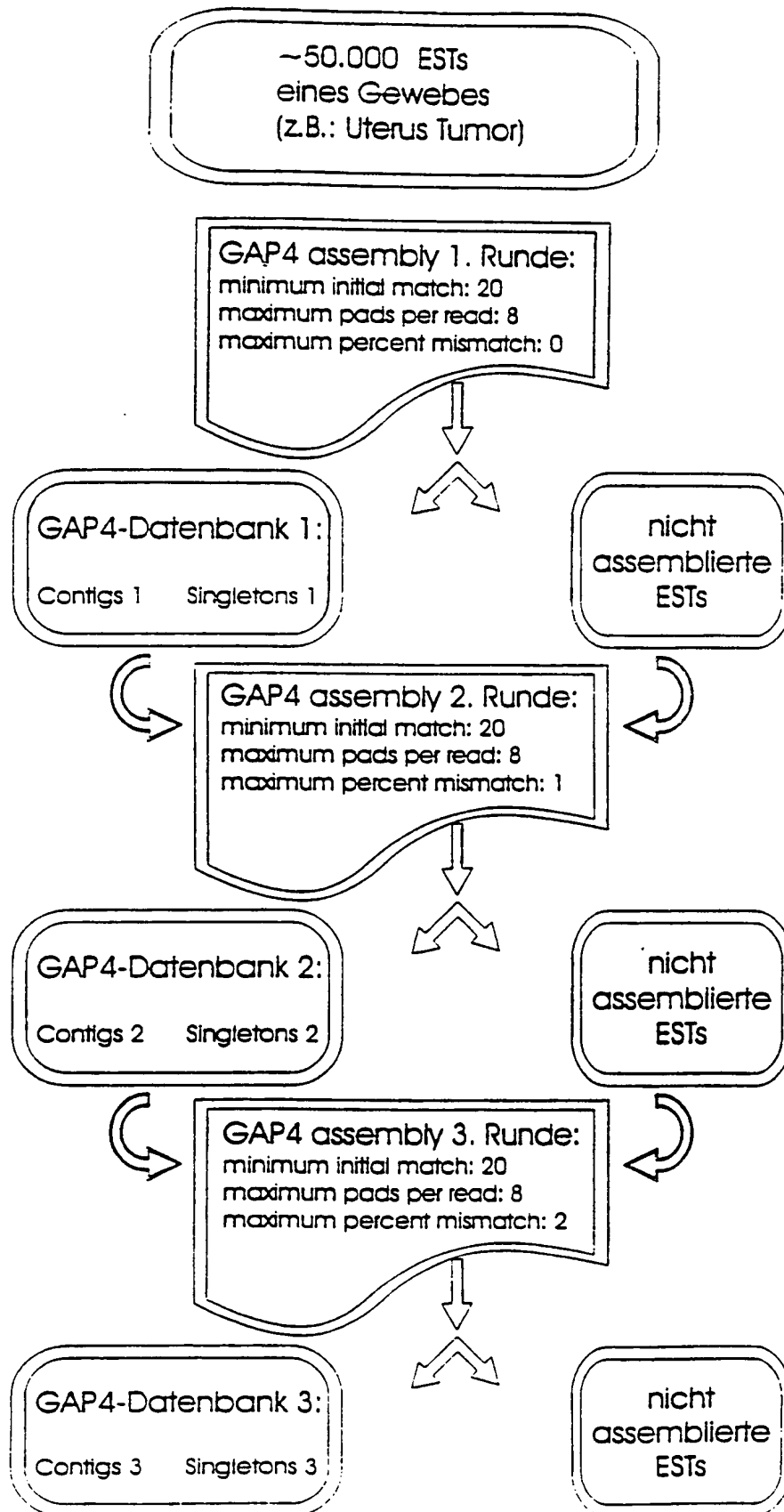


Fig. 2b1

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GAP4 Database 3:  
Contigs 3  
Singletons 3

unassembled  
ESTs

Consensus 3

GAP4 Assembly 4th Round:  
minimum initial match: 20  
maximum pads per read: 8  
maximum percent mismatch: 2

GAP4 Database 4:  
Contigs 4  
Singletons 4

unassembled  
ESTs

Consensus 4

GAP4 Assembly 5th Round:  
minimum initial match: 20  
maximum pads per read: 8  
maximum percent mismatch: 4

GAP4 Database 5:  
Contigs 5  
Singletons 5

unassembled  
ESTs 5

Consensus 5

Singletons 5

Figure 2b2

REPLACEMENT PAGE (RULE 26)

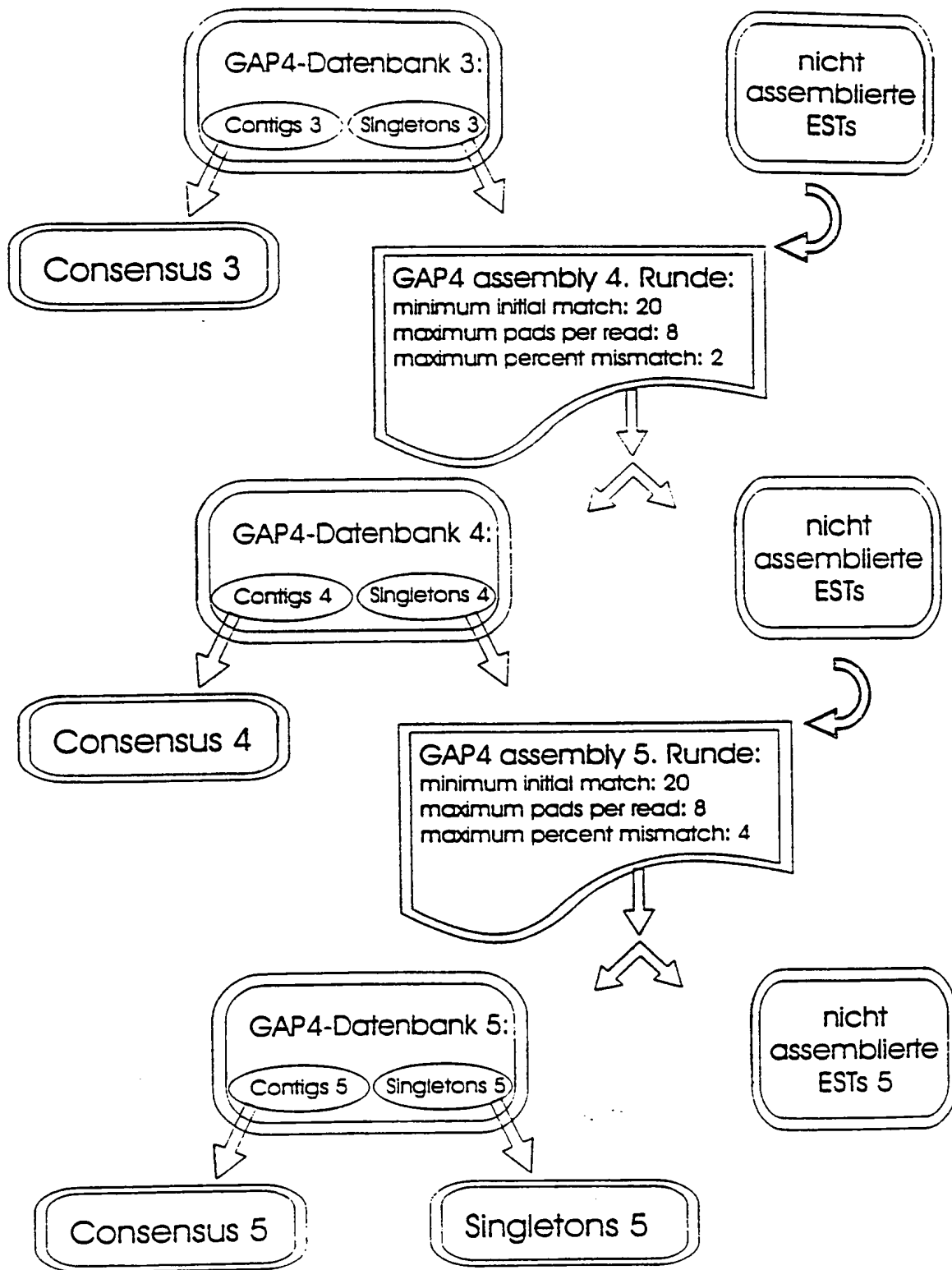


Fig. 2b2



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Consensus 3

Singletons 5

Consensus 4

unassembled  
ESTs 5

Consensus 5

GAP4 Assembly 6th Round:  
minimum initial match: 20  
maximum pads per read: 8  
maximum percent mismatch: 4

Assembled database  
of a specific tissue  
(e.g.: uterus tumor)

Figure 2b3

REPLACEMENT PAGE (RULE 26)

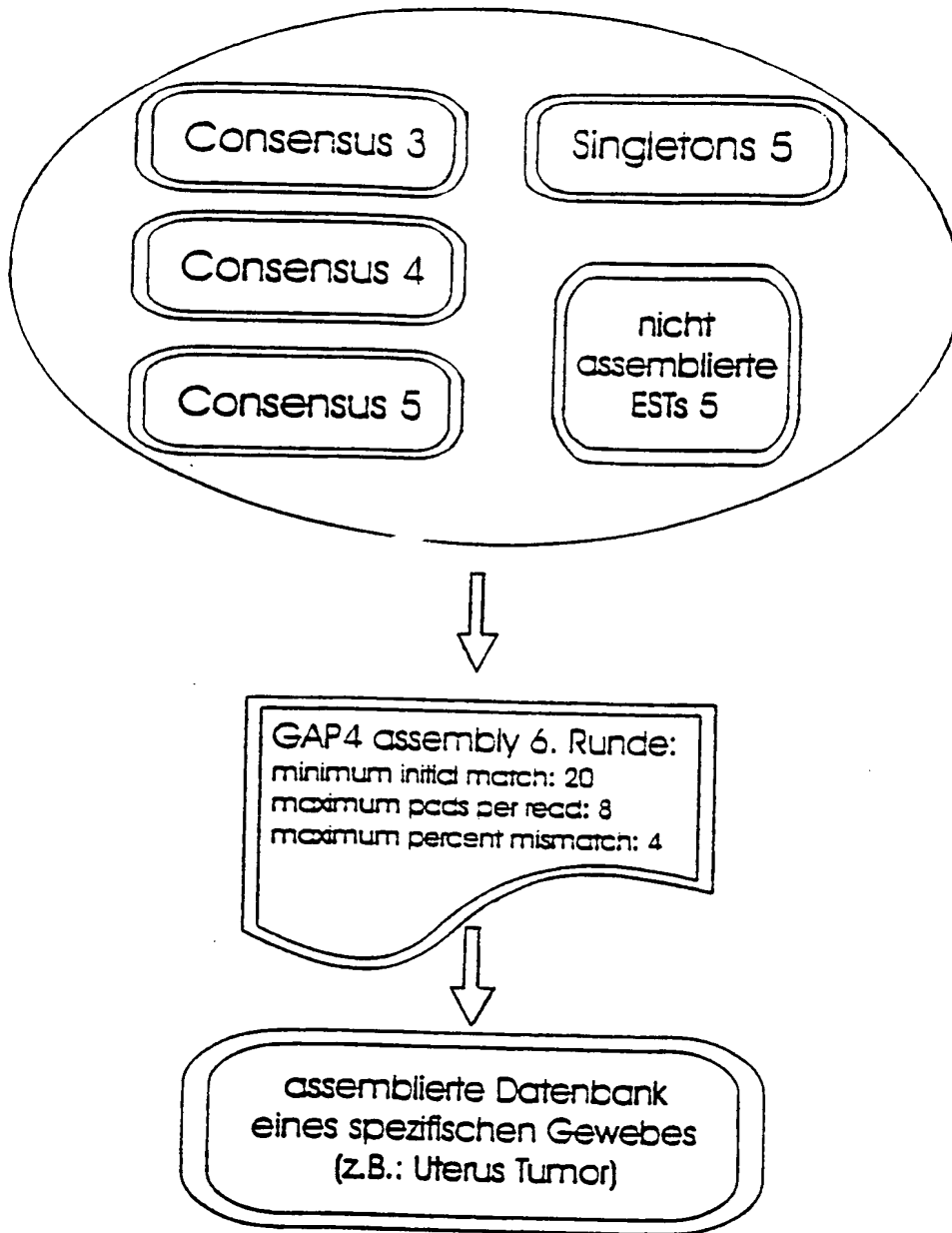


Fig. 2b3

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Assembled database  
of a specific tissue  
(e.g.: uterus tumor)

Consensus 6

Read-in as singletons

Database  
of a specific tissue  
(e.g.: uterus tumor)

Database of a second  
specific tissue  
(e.g.: normal uterus)

GAP4 Assembly  
minimum initial match: 20  
maximum pads per read: 8  
maximum percent mismatch: 4

Tumor tissue-  
specific ESTs

Non-tissue-  
specific ESTs

Normal tissue-  
specific ESTs

Fig. 2b4

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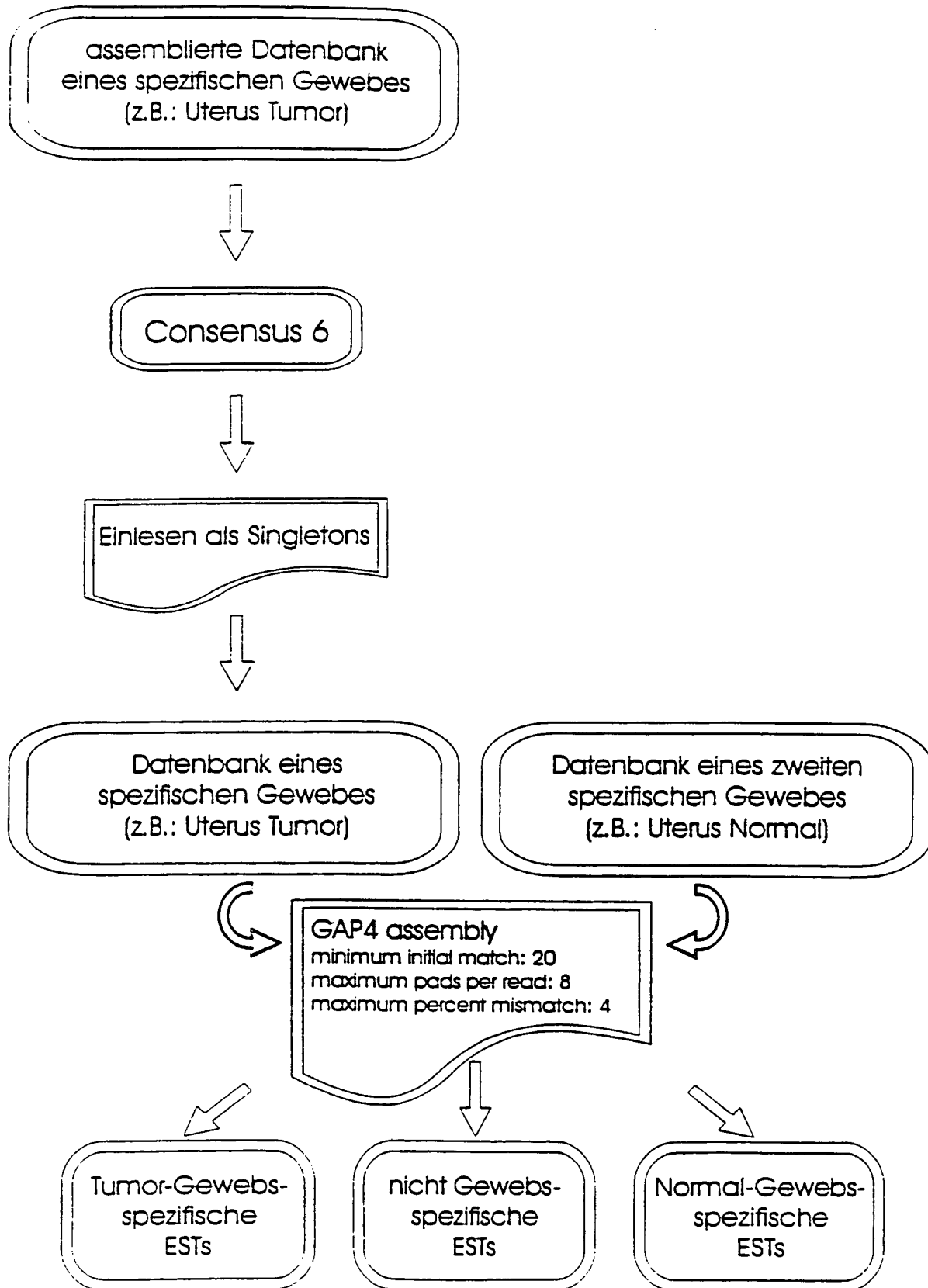


Fig. 2b4

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In silico subtraction of gene expression in various tissues

~30,000 consensus sequences  
normal tissue

~30,000 consensus sequences  
tumor tissue

Assembling at 4% mismatch

Normal tissue  
Specific genes

Cancer tissue  
Specific genes

Genes expressed in both tissues

Figure 3

REPLACEMENT PAGE (RULE 26)

# In silico Subtraktion der Genexpression in verschiedenen Geweben

~30.000 Konsensussequenzen  
Normalgewebe

~30.000 Konsensussequenzen  
Krebsgewebe

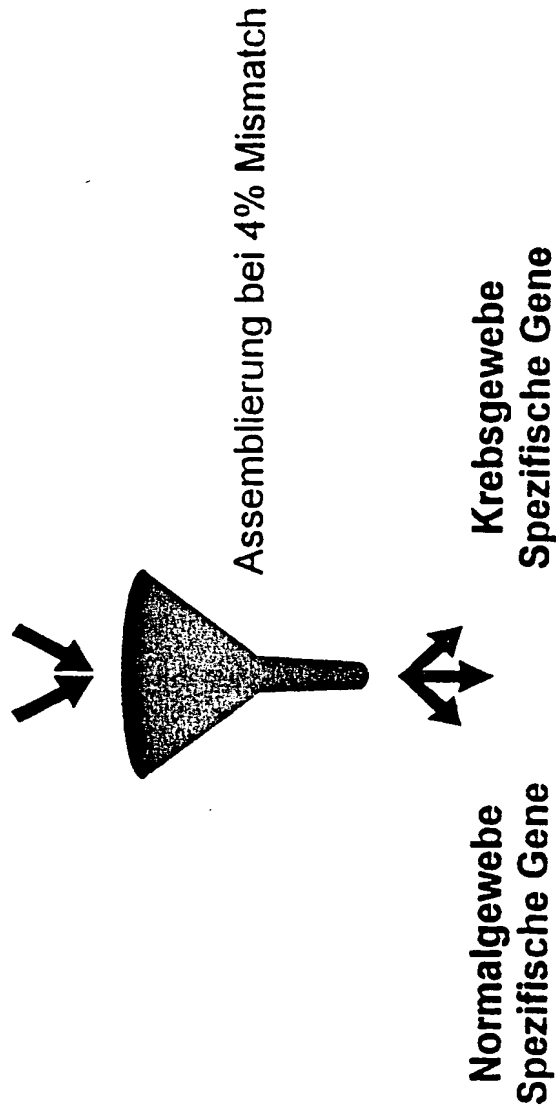


Fig. 3

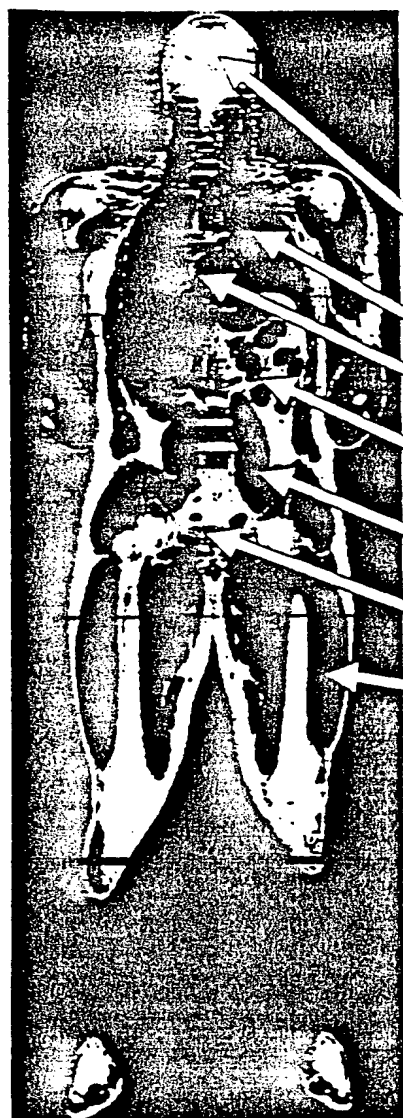
Genes of interest

Determination of tissue-specific expression  
via electronic Northern (INCYTE LifeSeq and  
public EST databases)

Candidate genes for tumor suppressors or  
tumor activators

Figure 4a

REPLACEMENT PAGE (RULE 26)



Gene von Interesse

Bestimmung der  
gewebsspezifischen  
Expression über  
elektronischen Northern  
( INCYTE LifeSeq und  
öffentliche EST  
Datenbanken)

Kandidatengene für  
Tumorsuppressoren oder  
Tumoraktivatoren

Fig. 4a



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Partial cDNA sequence  
e.g. EST or contig  
S

...GCCTCAAGTTATC...

WHILE  $C_i > C_{i-1}$ 

Electronic Northern Blot

Fisher's Exact Test IF  $H_0$  EXIT

Automatic Lengthening

Consensus sequence C

...ATGTCCTAGCCTCAAGTTATCAGATGCAA...

Figure 4b

REPLACEMENT PAGE (RULE 26)

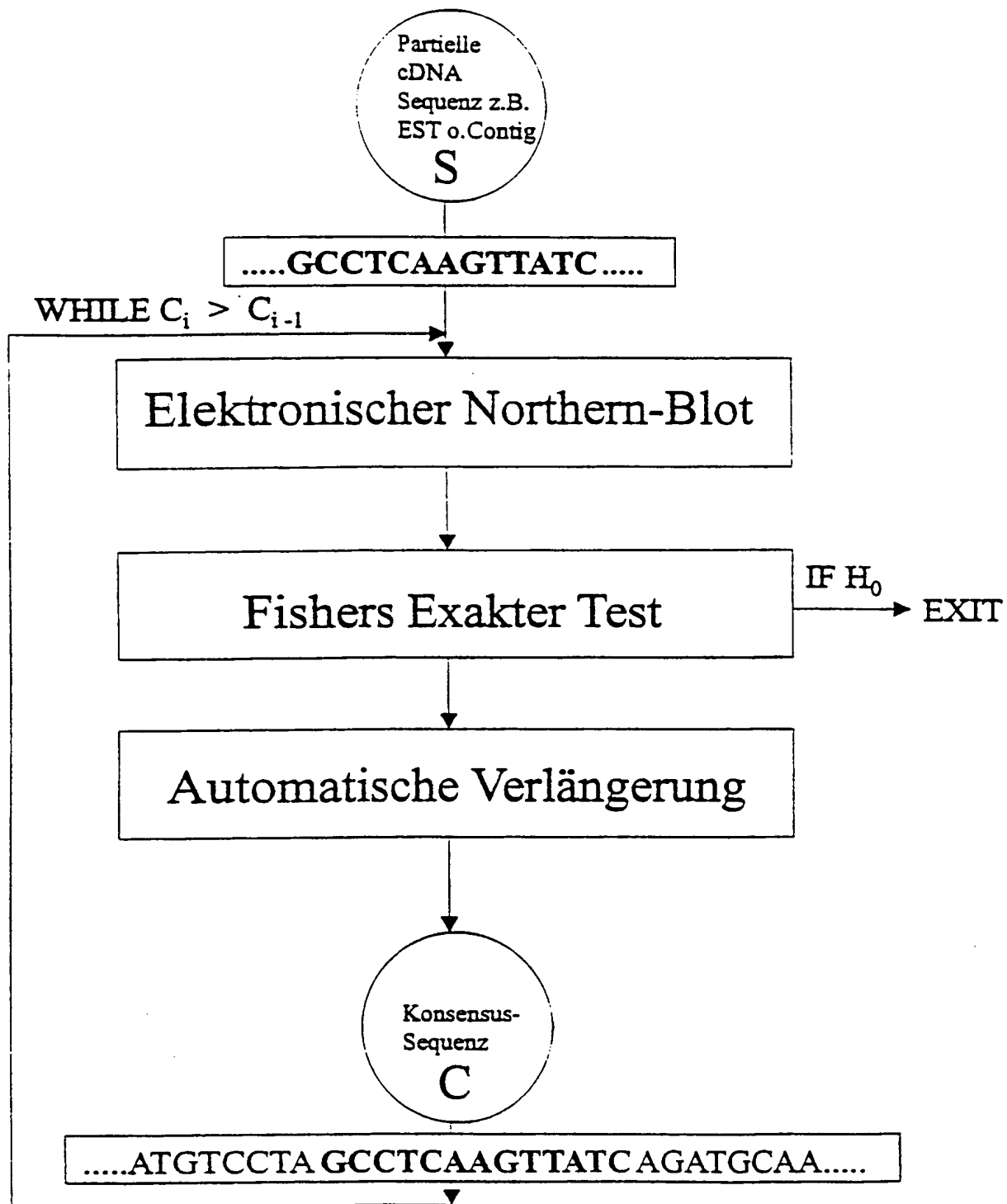


Fig. 4b

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Isolation of genomic BAC and PAC clones

Chromosomal clone localization via FISH

Hybridization signal

Sequencing of clones that are located in regions that have chromosomal deletions in prostate and breast cancer leads to identification of candidate genes

Exon          Intron

Confirmation of candidate genes by screening of mutations and/or deletions in cancer tissues

Figure 5

REPLACEMENT PAGE (RULE 26)

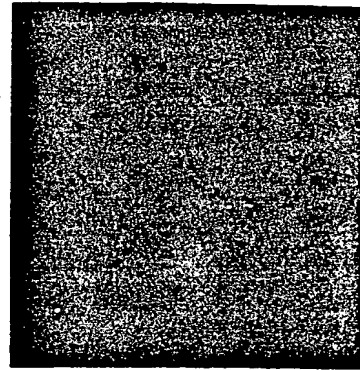
Isolieren von genomischen BAC und PAC Klonen



Chromosomale Klon-Lokalisation über FISH



Hybridisierungssignal



Sequenzierung von Klonen, die in Regionen lokalisiert sind, die chromosomale Deletionen in Prostata- und Brustkrebs aufweisen, führt zur Identifizierung von Kandidatengenen



Bestätigung der Kandidatengene durch Screening von Mutationen und/oder Deletionen in Krebsgeweben

Fig. 5